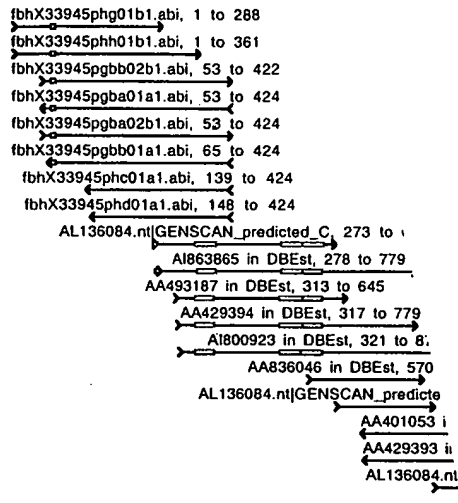


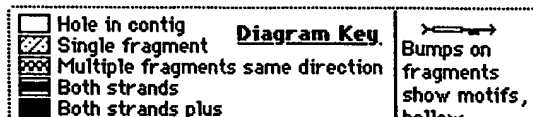
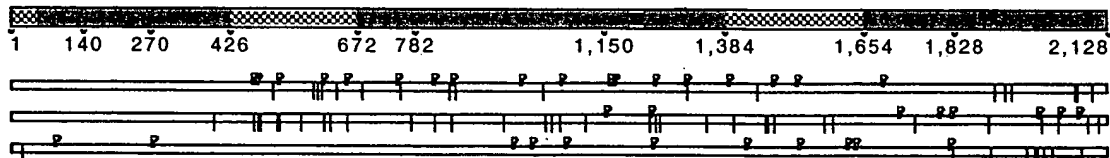
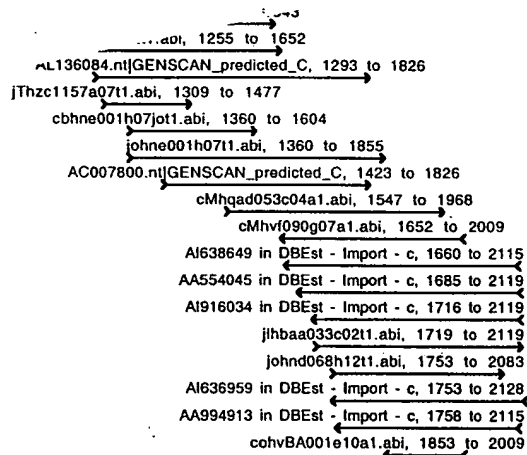
BEST AVAILABLE COPY

Exhibit B1 to Accompany Declaration under
37 CFR §1.131 for US Appln. No. 10/074,527

33945
Sequencher™ "33945"



*2 bp differences
that change amino acids
orthologs & genomic not
of great help. Decide
which to use - ph or pg.
Pete*



MI:fbhX33945pee03g1 (Human)**Description: Sample Information**

Name: fbhX33945pee03g1
Type: Full Length cDNA
Submitted on: Dec 12, 2000
NC project: Bayer
Species: Human
Tissue: unspecified
Internal id: 107050574

Sequence Information

Creation method: PhredBaseCall
Name: PHRED Base Calling Event
Created on: Dec 14, 2000
Created by: Pipeline
Accession number: (none)

Creation method: ABIBaseCall
Name: ABI Base Calling Event
Created on: Dec 14, 2000
Created by: Pipeline
Accession number: 107241068

Analyses: Note: Excludes periodic reanalysis events.

| Description | Date | Requested by | Sta |
|------------------------------|--------------|--------------|-----|
| <u>Internal Db Check</u> | Dec 14, 2000 | Pipeline | YE |
| <u>CUR Mildb Check</u> | Dec 15, 2000 | Pipeline | YE |
| <u>Nucleic Acid Db Check</u> | Dec 16, 2000 | Pipeline | YE |
| <u>Protein Db Check</u> | Dec 16, 2000 | Pipeline | YE |
| <u>DBEST Db Check</u> | Dec 16, 2000 | Pipeline | YE |
| <u>PDB Db Check</u> | Dec 16, 2000 | Pipeline | YE |
| <u>Signal Peptide Check</u> | Dec 16, 2000 | Pipeline | YE |
| <u>1.4 BLAST vs. PNU</u> | May 28, 2004 | Olga Tayber | SU |
| <u>1.4 BLAST vs. NUC</u> | May 28, 2004 | Olga Tayber | SU |

Base Array: **PHRED Base Call - complete**

Color and case key: NORMAL, low quality, vector, repeat

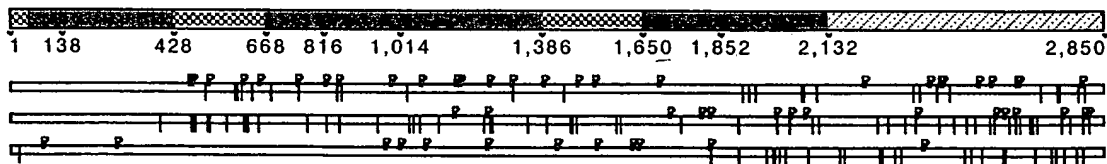
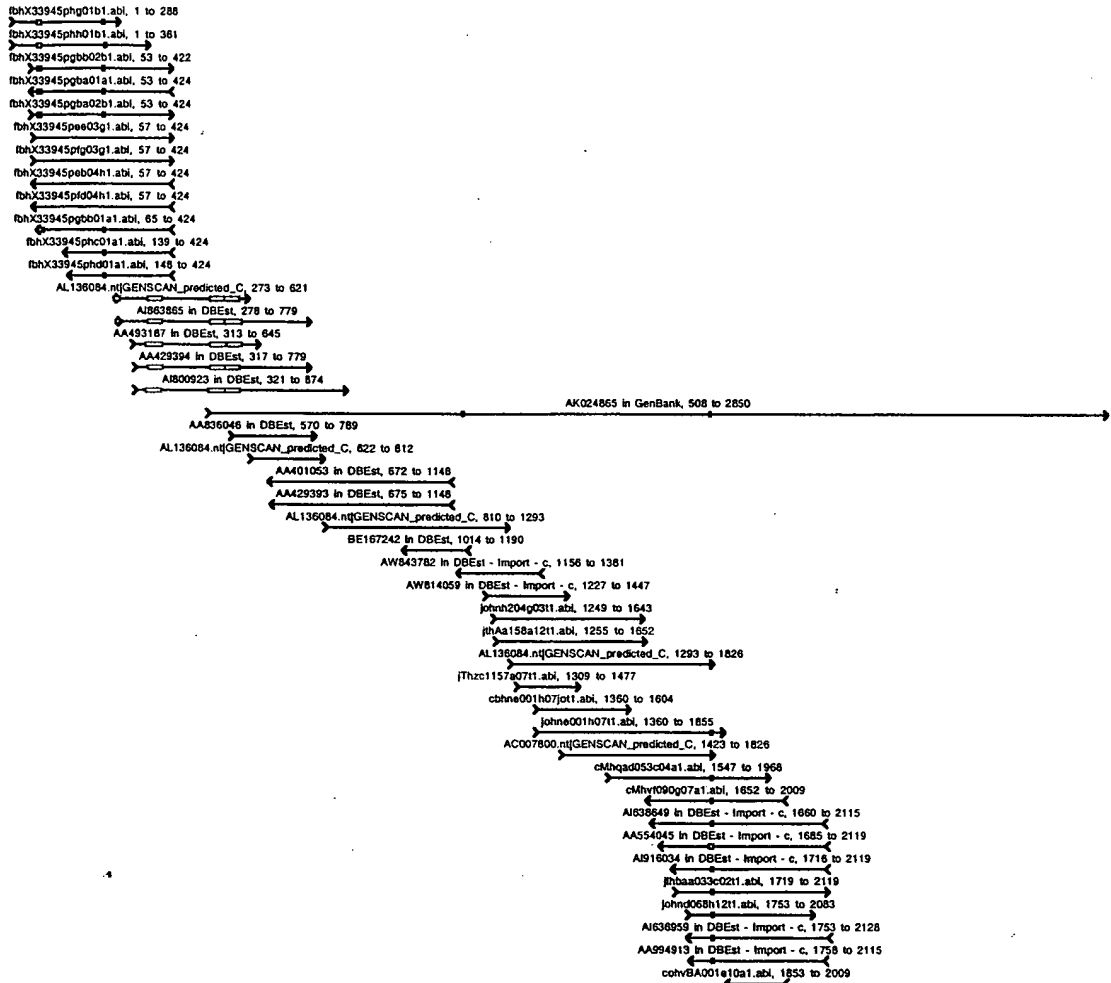
Ttgggtaccgggccccccctcgaggtcgacggtatcgataagcttgatatcgaattcctg
cagcccgggggatccgcccgcgcagaTCGCTGGCTGCAGTTGGCGGGCGCATGTGGGGGC
GCACGGCGCGGCGGCGCTGCCCCGCGGAAGTGGCGCGCGCCGGGAGGCGCTGTTGGTGC
TCCTGGCGCTACTGGCGTTGGCCGGGCTGGGCTCGGTGCTGCGGGCGCAGCGTGGGGCCG
GGGCCGGGCTGCCGAGCCGGGACCCCGCGCACCCCGCGCCCGGGCGGCGGAGCCGG

TCATGCCGCGGCCGCCGGTGCCGGCGAACGCGCTGGGCGCGCGGGGCGAGGCGGTGCGGC
TGCAGCTGCAGGGCGAGGAGCTGCGGCTGCAGGAGGAGAGCGTGCGGCTGCACCAGATTA
ACATCTACCTCAGCGACCGCATCTCACTGCACCGgggctagagcgccgccaccgcggtg
gagctccagcttttgttcccttagtgagggttaattgcgcgcttgcgtaatcatggtn

| Comments: | Author | Date | Comment |
|-------------|-------------|-------------|-------------|
| <div></div> | <div></div> | <div></div> | <div></div> |

33945
Sequencher™ "33945"

Exhibit B3 to Accompany Declaration under
37 CFR §1.131 for US Appln. No. 10/074,527



| Diagram Key | |
|-------------|---|
| | Hole in contig |
| | Single fragment |
| | Multiple fragments same direction |
| | Both strands |
| | Both strands plus |
| | Start codon frame 1 |
| | Stop codon frame 2 |
| | Bumps on fragments show motifs, hollow rectangles show features |

Sample Information

name: Fbh33945FL
type: Plain DNA Sequence
submitted on: December 18 2000
NC project: Bayer
species: Human
tissue: unspecified
internal id: 107445732
restrictions: none

**Exhibit B4 to Accompany Declaration under
37 CFR §1.131 for US Appln. No. 10/074,527**

Sequences Information

creation method: Loading
name: Load
created on: December 18 2000
created by: Peter Olandt
accession number: 107445733

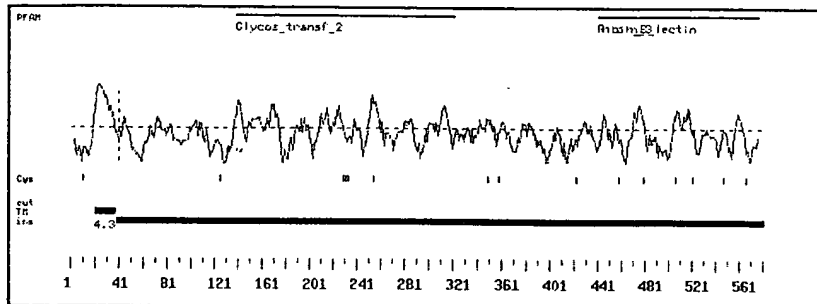
> Fbh33945FL - Import - complete

```
1      CCGGCTCGGT ACCACTATAA CGGCCGCCAG TGTGCTGGAA TTCGCCCTTG CGCAGATCGC
61     TGGCTGCAGT TGGCGGGCGC ATGTGGGGGC GCACGGCGCG GCGGCGCTGC CCGCGGGAAC
121    TGGCGCGCGG CCGGGAGGCG CTGTTGGTGC TCCTGGCGCT ACTGGCGTTG GCCGGGCTGG
181    GCTCGGTGCT GCGGGCGCAG CGTGGGGCCG GGGCCGGGGC TGCCGAGCCG GGACCCCGCG
241    GCACCCCGCG CCCCGGGCGG CGCGAGCCGG TCATGCCCGG GCCCGCGGTG CCGGCGAACG
301    CGCTGGGCGC GCGGGGCGAG GCGGTGCGGC TGCAGCTGCA GGGCGAGGAG CTGCGGCTGC
361    AGGAGGAGAG CGTGCGGCTG CACCAGATTA ACATCTACCT CAGCGACCGC ATCTCACTGC
421    ACCGCCGCCT GCCCGAGCGC TGAACCCGCG TGTGCAAAGA GAAGAAATAT GATTATGATA
481    ATTTGCCCAG GACATCTGTT ATCATAGCAT TTTATAATGA AGCCTGGTCA ACTCTCCTTC
541    GGACAGTTTA CAGTGTCTTT GAGACATCCC CGGATATCCT GCTAGAAGAA GTGATCCTTG
601    TAGATGACTA CAGTGATAGA GAGCACCTGA AGGAGCGCTT GGCCAATGAG CTTTCGGGAC
661    TGCCCAAGGT GCGCCTGATC CGCGCCAACA AGAGAGAGGG CCTGGTGCGA GCGCGGCTGC
721    TGGGGGCGTC TGGGCGGAGG GCGGATGTTT TGACCTTCCT GGAAGTGCAC TGTGAGTGCC
781    ACGAAGGGTG GCTGGAGCCG CTGCTGCAGA GGATCCATGA AGAGGAGTCG GCAGTGGTGT
841    GCGCGGTGAT TGATGTGATC GACTGGAACA CCTTCGAATA CCTGGGGAAC TCCGGGGAGC
901    CCCAGATCGG CGGTTTCGAC TGGAGGCTGG TGTTACAGTG GCACACAGTT CCTGAGAGGG
961    AGAGGATACG GATGCAATCC CCCGTCGATG TCATCAGGTC TCCAACAATG GCTGGTGGGC
1021   TGTTTGCTGT GAGTAAGAAA TATTTTGAAT ATCTGGGGTC TTATGATACA GGAATGGAAG
1081   TTTGGGGAGG AGAAAACCTC GAATTTTCCT TTAGGATCTG GCAGTGTGGT GGGGTTCTGG
1141   AAACACACCC ATGTTCCCAT GTTGGCCATG TTTTCCCAA GCAAGCTCCC TACTCCCGCA
1201   ACAAGGCTCT GGCCAACAGT GTTCGTGCAG CTGAAGTATG GATGGATGAA TTAAAGAGC
1261   TCTACTACCA TCGCAACCCC CGTGCCCGCT TGGAACCTTT TGGGGATGTG ACAGAGAGGA
1321   AGCAGTCCG GGACAAGCTC CAGTGTAAG ACTTCAAGTG GTTCTTGAG ACTGTGTATC
1381   CAGAACTGCA TGTGCCTGAG GACAGGCCTG GCTTCTCGG GATGCTCCAG AACAAAGGAC
1441   TAACAGACTA CTGCTTTGAC TATAACCTC CCGATGAAAA CCAGATTGTG GGACACCAGG
1501   TCATTCTGTA CCTCTGTCAT GGGATGGGCC AGAATCAGTT TTTCGAGTAC ACGTCCCAGA
```

1561 AAGAAATACG CTATAACACC CACCAGCCTG AGGGCTGCGT TGCTGTGGAA GCAGGAATGG
1621 ATACCCCTTAT CATGCATCTC TCGAAGAAA CTGCCCCAGA GAATCAGAAG TTCATCTTGC
1681 AGGAGGATGG ATCTTTATTT CACGAACAGT CCAAGAAATG TGTCCAGGCT GCGAGGAAGG
1741 AGTCGAGTGA CAGTTTCGTT CCACTCTTAC GAGACTGCAC CAACTCGGAT CATCAGAAAT
1801 GGTCTCTCAA AGAGCGCATG TTATGAAGCC TCGTGTATCA AGGAGCCCAT CGAAGGAGAC
1861 TGTGGAGCCA GGACTCTGCC CAACAAAGAC TTAGCTAAGC AGTGACCAGA ACCCACCAAA
1921 AACTAGGCTG CATTGCTTTG AAGAGGCAAT CATTTTGCCA TTTGTGAAAG TTGTGTGGA
1981 TTTAGTAAAA ATGTGAATAA GCTTTGTACT TATTTTGAGA ACTTTTTAAA TGTTCCAAAA
2041 TACCCTATTT TCAAAGGGTA ATCGTAAGAT GTTAACCCCTT GGTATTTAGA AAATTAAAAAC
2101 CTTATAATAT TTTTCTATCA ARAWRWAWAT TTTACAGTCG TGCCTTTTAC TCTCATTAGC
2161 AAAAAAGATA AAGATTTTAT TTTGGTATTT ACAAGAATTC CCAGGTACGA AGATATCTGC
2221 ATGGGTGGAA ATCAGGTTC AAGCAACGTAC TTTGCATTAA CTGATAATAC CTCAGCTGCG
2281 GGGTTAAAGT TTTCCAGTA TAGAGAGACT GTCAGTAGGA ACATTGTATT GATTTATTCA
2341 GGTCATTGAG ATCTTCTAGA TGTATTTTAA AAAGAATGCT TTTTGGTTAT GTGTTGCTAC
2401 CACAGTTAAC ACTCCATAAT GTTCATGTCA GCCAAAGAGG ACTAACCAAA GCTGAAATCT
2461 CAGAGAACAA TTTGCTTTAC TAAGCTGAGT CAACTTGAGA GCGAACTTCT AACAAATGCCG
2521 CACTGTAGTG TGGCTGGTTC TACCACTATG ACTTTAAAAC ATGTTTATAT CATTTTAAAT
2581 TTTTATGATA CGGTAGTGTC AGGGAGAAAT GTAATGTTCT ATATGAAATT CCTTTTCAA
2641 GTTTGTTTAT TAATAACAGT TATTAATTTA AATCAGCGTT AGAGTTGTG CTGCTGCAAC
2701 TGCTGTGAAA ATTTCTCTGA GTAATCTCTGA TTTGTGAATG ATCCCAGACC AACCTGAGA
2761 TTTTGTCAAC CTGATTAAAGT CAATATGAAT GATTAAAAAG ATGTGAGAAC AAAAAA
2821 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

[Back to orfanal.cgi](#)

Analysis of 33945 (581 aa)



>33945
MKRTARRRCPRELRGREGALLVLLALLAGLSVLRAGRGAGAGAAEPFPTPRGR
REPVMPPFPVPAALGARGAVRLQGEELRLQESVRLHQINILSDRI SLHRLPER
WNPCKEKKYDYNLPRTSVIIAFYNEAMSTLLRTVYSVLETSFDILLEEVILVDDYSDR
EHLKERLANELSGLPKVRILIRANKREGVLRARLLGASARGDVLTFDCHCECHGWLPE
LLQRIHEESAVVCPIVDIWMITFEYLGNSGEPQIGFDMRLVFTMTVPERIRMQS
PVDIRSPHAGLFAVSKKYPFYLGSYDTGNEVMGGENLEFSFRIMCGGVLETHPCSH
VGRVFPQAFYERKALANVRAAEVWDEFKELYTHSRARLEFPDPTERKOLRDL
QCKDFKFLTYVPELVPEDRPGFCHLQNGKLTQYCFDYPDPDENIYGHVILYLCN
GKGQHFETTSQKEIRYVTHQPEGCIAYAGHDTLLHLCETAPENQFLLQEDGSLF
HEQSKKCVQAARKSSDSFVPLLRDCTNSHQWFFKERGL

PSORT Prediction of Protein Localization

MITDISC: discrimination of mitochondrial targeting seq
A content: 8 Hyd Moment(75): 13.73
Hyd Moment(95): 16.65 G content: 2
D/E content: 2 S/T content: 1
Score: 1.89

Gavel: prediction of cleavage sites for mitochondrial preseq
R-2 motif at 19 RRC|PR

NUCDISC: discrimination of nuclear localization signals
pat4: none
pat7: PLCKEKK (3) at 123
bipartite: none
content of basic residues: 12.9%
NLS Score: -0.22

ER Membrane Retention Signals:
XXRR-like motif in the N-terminus: WGRT

KXXX-like motif in the C-terminus: KERM

Final Results (k = 9/23):

43.5 %: mitochondrial
30.4 %: cytoplasmic
8.7 %: vacuolar
8.7 %: nuclear
4.3 %: Golgi
4.3 %: endoplasmic reticulum

prediction for 33945 in mit (k=23)

| Start | End | Feature | Seq |
|-------|-----|----------------------------------|------------------------|
| 86 | 107 | Leucine zipper pattern (PS00029) | LQGEELRLQE...VRLHQINYL |

Signal Peptide Predictions for 33945

| Method | Predict | Score | Mat@ |
|---------------------|---------|-------|------|
| SignalP (eukaryote) | YES | | 40 |

Note: amino-terminal 70aa used for signal peptide prediction

Transmembrane Segments Predicted by MEMSAT

| Start | End | Orient | Score |
|-------|-----|----------|-------|
| 20 | 37 | out->ins | 4.3 |

>33945
MKRTARRRCPRELRGREGALLVLLALLAGLSVLRAGRGAGAGAAEPFPTPRGR
REPVMPPFPVPAALGARGAVRLQGEELRLQESVRLHQINILSDRI SLHRLPER
WNPCKEKKYDYNLPRTSVIIAFYNEAMSTLLRTVYSVLETSFDILLEEVILVDDYSDR
EHLKERLANELSGLPKVRILIRANKREGVLRARLLGASARGDVLTFDCHCECHGWLPE

http://range.mpi.com/seqs/Varlenal/33945_200308.html

LLQRIHEESAVKCPVIVIDWNTFEYLQNSCEPQIGFDMRLVFTWHTVPERERIRMQS
PVQVIRSPTHAGCLFAVSKRYFEYLGSYDTGMEHWGIDNLEFSFRIWCCGVLETHPCSH
VGHVFPKQAFYSRKALANSVRAAEVMMDEFKELYHNRPRARLEPPQDUTERKQLRDKL
QCKDFDMFLETVPFELHVPEDRPGFFQMLQNKGLTYHCFDYNPPDENQIVCHQVILYLCH
GHSQHQFFETTSQKEIRYNTHQPECCI AVEAGHDTLIMHLCEETAPEKQKFLQEDGSLP
HDSKMCVQAARAESSDSFVPLLRDCTNSDHQKQWFFKERHL

Transmembrane segments for presumed mature peptide

| Start | End | Orient | Score |
|-------|-----|--------|-------|
|-------|-----|--------|-------|

Prosite Pattern Matches for 33945

Prosite version: Release 12.2 of February 1995

>PS00004|PDOC00004|CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.

Query: 552 RKES 555

>PS00005|PDOC00005|PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.

Query: 5 TAR 7

Query: 55 TPR 57

Query: 97 SVR 99

Query: 108 SDR 110

Query: 178 SDR 180

Query: 318 SKK 320

Query: 343 SPR 345

Query: 380 SVR 382

Query: 411 TER 413

Query: 492 SQK 494

Query: 544 SKK 546

>PS00006|PDOC00006|CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.

Query: 158 SVLE 161

Query: 162 TSPD 165

Query: 178 SDRE 181

Query: 225 TPLD 228

Query: 289 TVPE 292

Query: 300 SPVD 303

Query: 330 TGME 333

Query: 492 SQKE 495

Query: 524 TAPE 527

Query: 567 TNSD 570

>PS00007|PDOC00007|TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.

Query: 426 KWFLETYY 433

>PS00008|PDOC00008|MYRISTYL N-myristoylation site.

Query: 42 GAGAGA 47

Query: 207 GLVRAR 212

Query: 215 GASAAAR 220

Query: 312 GGLFAV 317

Query: 326 GSYDTG 331

Query: 351 GVLETH 356

Query: 447 GMLQNK 452

Query: 481 GHSQHQ 486

>PS00009|PDOC00009|AMIDATION Amidation site.

Query: 58 PGRR 61

>PS00010|PDOC00010|RGD Cell attachment sequence.

Query: 220 RGD 222

>P500029|PDOC00029|LEUCINE_ZIPPER Leucine zipper pattern.

Query: 86 LQGEELRLQESVRLHQINIYL 107

Protein Family / Domain Matches, HMMer version 2

Searching for complete domains in PFAM
hmmpfam - search a single seq against HMM database
HMMER 2.1.1 (Dec 1998)
Copyright (C) 1992-1998 Washington University School of Medicine
HMMER is freely distributed under the GNU General Public License (GPL).

HMM file: /prod/dda/seqanal/PFAM/pfam5.5/pfam
Sequence file: /prod/dda/wspace/orfanal/oa-script.29948.seq
Query: 33945

| Model | Description | Score | E-value | N |
|-------------------|--------------------------------------|-------|---------|---|
| Glycosyl_transf_2 | Glycosyl transferases | 85.1 | 1.4e-21 | 1 |
| Ricin_B_lectin | Similarity to lectin domain of ricin | 18.7 | 0.0016 | 1 |

| Model | Domain | seq-f | seq-t | hmm-f | hmm-t | score | E-value |
|-------------------|--------|-------|-------|-------|-------|-------|---------|
| Glycosyl_transf_2 | 1/1 | 139 | 322 | 1 | 187 | 85.1 | 1.4e-21 |
| Ricin_B_lectin | 1/1 | 441 | 577 | 1 | 145 | 18.7 | 0.0016 |

Alignments of top-scoring domains:
Glycosyl_transf_2: domain 1 of 1, from 139 to 322: score 85.1, E = 1.4e-21
*--siviptYNeedyLeelleSvIags.tledieivVDdGSetDetve
s+1+ YNe+...L+... SvI+ s+... e+i VDD S+...
33945 139 SVIIAPYNEAWSTLRTVYVLETSpDILLLEVILVDVYSREHLKE 185

iaedyIderikeenpriiivirleensgGpaArnkGirratGdsdyIlf
++ 1 ++ p+...ir ++ G ++Ar +g ++aGd ++f
33945 186 RLANEL-----SGLPK-VRLIRANKRE-GLVRARILGASARCD--VLTF 226

LDaDiftpdhkleklidyeeatdaavlgaida....yeyaegeenly.
LD+...++lel+... + m+... id+...eey+...
33945 227 LQNCCEHGMLEPLQRIHEESAVVCVVIDVIdmtFEYLGNSCEPQI 276

riaradterslfagllrktgrltgglelsfeigsnaIyrreafelf<--
33945 277 GGFNWLVTWVTWTFPERIRMGSP-VDIRSPHAGGLFAVSKXYF 322

Ricin_B_lectin: domain 1 of 1, from 441 to 577: score 18.7, E = 0.0016
*-->revfiviciI.vnmagrcIDvnsesedG...ngvqlwnChsnpgknQ
++ + 1+ g ++ C D n ++e+ + qv 1 Ch+ +g nQ
33945 441 DRPOFFGHLgKGLTDYCFDYNPPDENQIVgHQVILYLCHG-MEDNQ 486

KwsltYdaedgeirs.vvnnkCLtnanspgseVkiyGdsatsdnQKW
+ t a +eir + + +C +v+ + + + C ++ +nQ+
33945 487 FFETV---SQKEIRYnthQPEGCIAVEAGMDT--LIMHLCEETAPENQKF 531

elnndgllgnklllnlvntglvldvkgadtqngTklilytcsggrnqgWl
l dg++ ++ +...++ + + 1++c++ +g+W
33945 532 ILQEDGSLPH-----EQSKKCVQARKESDSFVPLLRDCTNSDHQKWF 575

pt<--
33945 576 FK 577

//
Searching for complete domains in SMART
hmmpfam - search a single seq against HMM database
HMMER 2.1.1 (Dec 1998)
Copyright (C) 1992-1998 Washington University School of Medicine
HMMER is freely distributed under the GNU General Public License (GPL).
HMM file: /ddm/robison/smart/smart/smart.all.hmm
Sequence file: /prod/dda/wspace/orfanal/oa-script.29948.seq
Query: 33945

| Model | Description | Score | E-value | N |
|---------|-------------|-------|---------|---|
| ricin_3 | | 73.3 | 5.1e-18 | 1 |

| Model | Domain | seq-f | seq-t | hmm-f | hmm-t | score | E-value |
|---------|--------|-------|-------|-------|-------|-------|---------|
| ricin_3 | 1/1 | 445 | 577 | 1 | 135 | 73.3 | 5.1e-18 |

Alignments of top-scoring domains:
ricin_3: domain 1 of 1, from 445 to 577: score 73.3, E = 5.1e-18
*-->rgyfliligtglCLdvngmsesksdGnpvqlwdChg.gmqlWkl
++ +1+ g t+ C d+n +e+ G ++v1+ Chg g nQ + +t
33945 445 FPQMLQNGGLTYCFDYNPPDENQIVgHQVILYLCHGmGQNFPEYT 491






Yneadgaiki...nsdlCLvng...ivtlyscDgttdkgnchQlWemkhd
g++ir +...++ C v ++ +t+ + C+ t + +nQ+ ++ d
33945 492 ---SQKEIRYnthQPEGCIAVEAGMDTLIMHLCEET--APENQKFILQED 536

gtirmpknakkgvdsglcldvkdgn....kvqlwtengsdapnQKwif
g + + +g +...++ + 1++c++ +nQK f+
33945 537 GSLPHE-----QSKKCVQARKESdsfVPLLRDCTNS--DHQKWF 577

<--
33945 - -

//

ProDom Matches

| ProdomId | Start | End | Description | Score |
|--|-------|-----|--|-------|
| View Prodom 2681  | 101 | 138 | p99.2 (20) PAGT(3) // TRANSFERASE N-ACETYL GALACTOSAMINYLTRANSFERASE POLYPEPTIDE ACETYL GALACTOSAMINYLTRANSFERASE UDP-GALNAC:POLYPEPTIDE GLYCOSYLTRANSFERASE PROTEIN-UDP PROTEIN- UDP N- | 99 |
| View Prodom 137344  | 108 | 187 | p99.2 (1) O44164_CAEEL // COSMID F16B3 | 74 |
| View Prodom 93  | 139 | 285 | p99.2 (314) NODC(8) PAGT(3) CAG2(3) // PROTEIN TRANSFERASE GLYCOSYLTRANSFERASE PUTATIVE BIOSYNTHESIS GLYCOSYL SYNTHASE TRANSMEMBRANE N-ACETYL GALACTOSAMINYLTRANSFERASE MEMBRANE | 108 |
| View Prodom 2308  | 287 | 443 | p99.2 (23) PAGT(3) // N-ACETYL GALACTOSAMINYLTRANSFERASE TRANSFERASE POLYPEPTIDE ACETYL GALACTOSAMINYLTRANSFERASE UDP-GALNAC:POLYPEPTIDE GLYCOSYLTRANSFERASE PROTEIN-UDP PROTEIN- UDP N- | 566 |
| View Prodom 617  | 453 | 574 | p99.2 (70) PAGT(3) ABFB(2) E13B(2) // SIGNAL HYDROLASE PRECURSOR TOXIN RRNA N-GLYCOSIDASE GLYCOSIDASE LECTIN REPEAT GLYCOPROTEIN | 104 |
| ProdomId | Start | End | Description | Score |

View Prodom 2308   

>2308 p99.2 (23) PAGT(3) // N-ACETYL GALACTOSAMINYLTRANSFERASE TRANSFERASE
POLYPEPTIDE ACETYL GALACTOSAMINYLTRANSFERASE UDP-GALNAC:POLYPEPTIDE
GLYCOSYLTRANSFERASE PROTEIN-UDP PROTEIN- UDP N-
Length = 172

Score = 566 (204.3 bits), Expect = 3.3e-55, P = 3.3e-55
Identities = 102/166 (61%), Positives = 128/166 (77%)

Query: 287 WHVPERERIRHQS-PVDVIRSPTHAGGLFAVSKKYFYLGSYDCHVWGGDLELSPR 345
WH VPE ER R + P D IRSPTHAGGLFA+K+YFE LG+YD CH+WGGINLE SFR
Sbjct: 2 WHVPEERKRRUKDPTDPIRSPTHAGGLFAINKEYFEELGYDPCMDMGGINLELSPR 61

Query: 346 IMQCGVLETHPCERVGVVFPQAPYS-----RKKALANSVRAAEVWDEKELYIHR 398
+MQCG L E PCSHVGHT K+P+ ** N+VR AEVWD+KE +Y
Sbjct: 62 VMQCGRLIVPCSHVGHVFKRSPYTFPGKSGKDVISRTVRAEVWDEYKEYFYKH 121

Query: 399 NPRAR-LEPPGVTERKQLRDKLOCKDFKMFLETVYFELHVPEDRP 443
NP+AR + PGD+ERK+LR+KLQCK FKM+LE VIP+L+VP P
Sbjct: 122 NPQARKVRDPSISERKELRKLQCKSPKNYLENVYDLYVFAHEP 167

View Prodom 617 

>617 p99.2 (70) PAGT(3) ABFB(2) E13B(2) // SIGNAL HYDROLASE PRECURSOR TOXIN
RRNA N-GLYCOSIDASE GLYCOSIDASE LECTIN REPEAT GLYCOPROTEIN
Length = 140

Score = 104 (41.7 bits), Expect = 3.1e-05, P = 3.1e-05
Identities = 29/128 (22%), Positives = 55/128 (42%)

Query: 453 GLTDYCFDYNFPDENQVGHQVILYLCHQM-CQNOFFEYTSQKEIRYNTNQPEGCI AVEA 511
G C D N + + G+ V L+ CH G NQ + + + IR N + + + C+
Sbjct: 11 GNNKGLDNDGNTVLDGNFVQMWQCHNWKGNQONTFNTDGTIRSNKQKX-CLTSSG 69

Query: 512 ----GMDLIMHLCEETAFENKRFILQEDGSLFHE-OSKCKVQAARKESSDSFVPLLRDC 566
G +I + MGR+ DG+ S C+ R + + + + + C
Sbjct: 70 YSPVGSVMVYNCHSAKNDNQKMEFNSDOTIIONPHSLCLDAYSDDTANGTKIMVYTC 129

Query: 567 TNSDHQKW 574
+ + O+W
Sbjct: 130 MGNNSQOM 137

View Prodom 2681

>2681 p99.2 (20) PAGT(3) // TRANSFERASE N-ACETYL GALACTOSAMINYLTRANSFERASE
POLYPEPTIDE ACETYL GALACTOSAMINYLTRANSFERASE UDP-GALNAC:POLYPEPTIDE
GLYCOSYLTRANSFERASE PROTEIN-UDP PROTEIN- UDP N-
Length = 118

Score = 99 (39.9 bits), Expect = 0.00011, P = 0.00011
Identities = 21/39 (53%), Positives = 27/39 (69%)

Query: 101 HQNIYLSDRISLHRLPKNPLCKEKYD-VNKLPT 138
+O N+Y SD ISL+R LP+ CK +KY+ YNKL P
Sbjct: 80 HQFNLYASDMISLRLPDKPECKTKYNFYDNLPTT 118

View Protein 93    

>93 p99.2 (314) NODC(8) PAGT(3) CAG2(3) // PROTEIN TRANSFERASE
GLYCOSYLTRANSFERASE PUTATIVE BIOSYNTHESIS GLYCOSYL SYNTHASE TRANSMEMBRANE
N-ACETYLGLUCOSAMINYLTTRANSFERASE MEMBRANE
Length = 196

Score = 108 (43.1 bits), Expect = 0.00056, P = 0.00056
Identities = 46/163 (28%), Positives = 74/163 (45%)

Query: 139 SVIIAFYNAMSTLLRTVYVLETSPD--ILLEEVILVDDYS-DR--EHLKE-RLANELS 192
SVII YNE S L V SVL+ + +EE+VDD S D E +E + E
Sbjct: 3 SVIIPTYNREESILKTLVSSVLQQYDNYEMEEIIIVDDGSTNTAEIVEEYSYSAKE 62

Query: 193 GLPKVRLIRANKREXXXXX-----XXXXXXXXXXDLTFLOCHCECHG--WLEPLLQ 243
KV++IR K + + + + + D + FLO + M WLE L++
Sbjct: 63 SRVKVKVIRNEKNSGMSAMNKGKLGKLGSGADQDIIDYIVFLDSD-DVHMSPNLEKLE 121

Query: 244 RIHEESAVVCPVIDIDMNYFEYLGNSGEPOI--GGFDMRLVF 285
+ E+ + VV V++ + +Y + + GG++W +++
Sbjct: 122 AMEEDNADVVGSRQVVNDENKQYSSATRLIHMEGTYNMSHY 164

View Protein 137344    

>137344 p99.2 (1) O44164_CAEEL // COSMID F16B3
Length = 196

Score = 74 (31.1 bits), Expect = 4.9, P = 0.99
Identities = 23/80 (28%), Positives = 41/80 (51%)

Query: 108 SDRISLRRLPERNNPLCKKKYDYDNLPRTSVIIAFYNAMSTLLRTVYVLETSPDIL 167
S + + R P+R PL R + D D L RTS + + WS+L + + + + DI+
Sbjct: 8 SSTVKSFRSKPKR-PFLAGQTVDEALSRTSNGHDKKREMSLL-SNRTKSKFDII 65

Query: 168 LEEVILVDDYSDEHLKERL 187
E + + + + R L ER+
Sbjct: 66 GERLTIEDQINSRLALLERV 85

Docket No. MPI01-018P1RNM

U.S. Serial No. 10/074,527, Filed February 12, 2002

EXHIBITS I – III

- Exhibit I: U.S. Provisional Application No. 60/254,308, filed December 8, 2000,
by Sanjanwala et al. (entire file history document)
- Exhibit II U.S. Provisional Application No. 60/256,189, filed December 15, 2000,
by Ding et al. (entire file history document)
- Exhibit III U.S. Provisional Application No. 60/203,331, filed May 11, 2000,
by Hassen et al. (entire file history document)

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